

SEQUENCE LISTING

<110> Sticklen, Masomeh B
 Maqbool, Shahina B
 Dale, Bruce E

<120> TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH
 DEGRADE
 LIGNIN AND CELLULOSE TO FERMENTABLE SUGARS

<130> MSU 4.1-539

<150> 60/242,408

<151> 2000-10-20

<160> 19

<170> PatentIn version 3.1

<210> 1

<211> 1110

<212> DNA

<213> Oryza sativa

<400> 1

```

gggtcggaga tgccaccacg gccacaaccc acgagcccgg cgcgacacca ccgcgcgcgt    60
tgagccagcc acaaacgccc gcggataggg gcgccgcacg cggccaatcc taccacatcc    120
ccggcctccg cggctcgagc gccgtgccat ccgatccgct gagttttggc tatttatacg    180
taccgcggga gcctgtgtgc agagagtgc tctcaagaag tactcgagca aagaaggaga    240
gagcttggtg agctgcagag atggccccct ccgtgatggc gtcgtcggcc accaccgtcg    300
ctcccttcca gggctcaagt ccaccgccgg catgccgtcg cccgccgtcc gaactccagc    360
ttcggcaacg tcagcatggc ggcaggatca ggtgcatgca ggtaattacc tactgatcca    420
acacacattc ttcttcttct tcttcttctt aaccaacatt aaccaacaac tcaattatcg    480
tttattcatt gaggtgtggc cgattgaggg catcaagaag ttcgagaccc tctcctacct    540
gccaccgctc accgtggagg acctcctgaa gcagatcgag tacctagctc cgttccaagt    600
ggtgccctgc ctcgagttca gcaaggctcg atttgtctac cgtgagaacc acaagtcccc    660
tggatactac gacggcaggt actggacat gtggaagctg cccatgttcg ggtgcaccga    720
cgccaccag gtcgtcaagg agctcgagga ggccaagaag gcgtaccctg atgcattcgt    780
ccgtatcatc ggcttcgaca acgttaggca ggtgcagctc atcagottca tcgcctacaa    840
cccgggctgc gaggagtctg gtggcaacta agccgtcatc gtcatatata gcctcgttta    900
attgttcata tctgattcga tgatgtctcc caccttgttt cgtgtgttcc cagtttgttt    960
catcgtcttt tgattttacc ggccgtgctc tgcttttggt ttttcttttc acctgattct   1020
ctctctgact tgatgtaaga gtggtatctg ctacgactat atgttgtttg ggtgaggcat   1080

```

atgtgaatga aatctatgaa agctccggct

1110

<210> 2
<211> 38
<212> PRT
<213> Oryza sativa

<400> 2

Met Ala Pro Ser Val Met Ala Ser Ser Ala Thr Thr Val Ala Pro Phe
1 5 10 15

Gln Gly Ser Ser Pro Pro Pro Ala Cys Arg Arg Pro Pro Ser Glu Leu
20 25 30

Gln Leu Arg Gln Arg Gln
35

<210> 3
<211> 6
<212> PRT
<213> synthetic peptide

<220>
<221> SIGNAL
<222> (1)..(6)
<223> targets the peroxisomes of plants

<400> 3

Arg Ala Val Ala Arg Leu
1 5

<210> 4
<211> 3004
<212> DNA
<213> Acidothermus cellulolyticus

<220>
<221> CDS
<222> (824)..(2512)
<223> E I beta-1,4-endoglucanase precursor

<400> 4

ggatccacgt tgtacaaggt cacctgtccg tcgttctggt agagcggcgg gatggtcacc 60
cgacgatct ctcttttgtt gatgtcgacg gtcacgtggt tacggtttgc ctcggccgcg 120
attttcgcgc tcgggcttgc tccggctgtc gggttcgggt tggcgtggtg tgcggagcac 180
gccgaggcga tcccaatgag ggcaaggcca agagcggagc cgatggcacg tcgggtggcc 240
gatgggggtac gccgatgggg cgtggcggtcc ccgccgcgga cagaaccgga tgcggaatag 300
gtcacgggtgc gacatgttgc cgtaccgcgg acccgatga caaggttggg tgcgcgggtc 360
gcctgtgagc tgccggctgg cgtctggatc atgggaacga tcccaccatt ccccgcaatc 420

gacgcgatcg ggagcagggc ggcgcgagcc ggaccgtgtg gtcgagccgg acgattcgcc	480
catacgggtgc tgcaatgccc agcgccatgt tgtcaatccg ccaaatgcag caatgcacac	540
atggacaggg attgtgactc tgagtaatga ttggattgcc ttcttgccgc ctacgcgtta	600
cgcagagtag gcgactgtat gcggtagggt ggcgctccag ccgtgggctg gacatgcctg	660
ctgcgaactc ttgacacgtc tggttgaacg cgcaatactc ccaacaccga tgggatcggt	720
cccataagtt tccgtctcac aacagaatcg gtgcgcctc atgatcaacg tgaaaggagt	780
acggggggaga acagacgggg gagaaaccaa cggggggattg gcg gtg ccg cgc gca	835
Val Pro Arg Ala	
1	
ttg cgg cga gtg cct ggc tgc cgg gtg atg ctg cgg gtc ggc gtc gtc	883
Leu Arg Arg Val Pro Gly Ser Arg Val Met Leu Arg Val Gly Val Val	
5 10 15 20	
gtc gcg gtg ctg gca ttg gtt gcc gca ctc gcc aac cta gcc gtg ccg	931
Val Ala Val Leu Ala Leu Val Ala Ala Leu Ala Asn Leu Ala Val Pro	
25 30 35	
cgg ccg gct cgc gcc gcg ggc ggc ggc tat tgg cac acg agc ggc cgg	979
Arg Pro Ala Arg Ala Ala Gly Gly Gly Tyr Trp His Thr Ser Gly Arg	
40 45 50	
gag atc ctg gac gcg aac aac gtg ccg gta cgg atc gcc ggc atc aac	1027
Glu Ile Leu Asp Ala Asn Asn Val Pro Val Arg Ile Ala Gly Ile Asn	
55 60 65	
tgg ttt ggg ttc gaa acc tgc aat tac gtc gtg cac ggt ctc tgg tca	1075
Trp Phe Gly Phe Glu Thr Cys Asn Tyr Val Val His Gly Leu Trp Ser	
70 75 80	
cgc gac tac cgc agc atg ctc gac cag ata aag tcg ctc ggc tac aac	1123
Arg Asp Tyr Arg Ser Met Leu Asp Gln Ile Lys Ser Leu Gly Tyr Asn	
85 90 95 100	
aca atc cgg ctg ccg tac tct gac gac att ctc aag ccg ggc acc atg	1171
Thr Ile Arg Leu Pro Tyr Ser Asp Asp Ile Leu Lys Pro Gly Thr Met	
105 110 115	
ccg aac agc atc aat ttt tac cag atg aat cag gac ctg cag ggt ctg	1219
Pro Asn Ser Ile Asn Phe Tyr Gln Met Asn Gln Asp Leu Gln Gly Leu	
120 125 130	
acg tcc ttg cag gtc atg gac aaa atc gtc gcg tac gcc ggt cag atc	1267
Thr Ser Leu Gln Val Met Asp Lys Ile Val Ala Tyr Ala Gly Gln Ile	
135 140 145	
ggc ctg cgc atc att ctt gac cgc cac cga ccg gat tgc agc ggg cag	1315
Gly Leu Arg Ile Ile Leu Asp Arg His Arg Pro Asp Cys Ser Gly Gln	
150 155 160	
tcg gcg ctg tgg tac acg agc agc gtc tcg gag gct acg tgg att tcc	1363
Ser Ala Leu Trp Tyr Thr Ser Ser Val Ser Glu Ala Thr Trp Ile Ser	
165 170 175 180	
gac ctg caa gcg ctg gcg cag cgc tac aag gga aac ccg acg gtc gtc	1411
Asp Leu Gln Ala Leu Ala Gln Arg Tyr Lys Gly Asn Pro Thr Val Val	
185 190 195	

ggc ttt gac ttg cac aac gag ccg cat gac ccg gcc tgc tgg ggc tgc	1459
Gly Phe Asp Leu His Asn Glu Pro His Asp Pro Ala Cys Trp Gly Cys	
200 205 210	
ggc gat ccg agc atc gac tgg cga ttg gcc gcc gag cgg gcc gga aac	1507
Gly Asp Pro Ser Ile Asp Trp Arg Leu Ala Ala Glu Arg Ala Gly Asn	
215 220 225	
gcc gtg ctc tcg gtg aat ccg aac ctg ctc att ttc gtc gaa ggt gtg	1555
Ala Val Leu Ser Val Asn Pro Asn Leu Leu Ile Phe Val Glu Gly Val	
230 235 240	
cag agc tac aac gga gac tcc tac tgg tgg ggc gcc aac ctg caa gga	1603
Gln Ser Tyr Asn Gly Asp Ser Tyr Trp Trp Gly Gly Asn Leu Gln Gly	
245 250 255 260	
gcc gcc cag tac ccg gtc gtg ctg aac gtg ccg aac cgc ctg gtg tac	1651
Ala Gly Gln Tyr Pro Val Val Leu Asn Val Pro Asn Arg Leu Val Tyr	
265 270 275	
tcg gcg cac gac tac gcg acg agc gtc tac ccg cag acg tgg ttc agc	1699
Ser Ala His Asp Tyr Ala Thr Ser Val Tyr Pro Gln Thr Trp Phe Ser	
280 285 290	
gat ccg acc ttc ccc aac aac atg ccc ggc atc tgg aac aag aac tgg	1747
Asp Pro Thr Phe Pro Asn Asn Met Pro Gly Ile Trp Asn Lys Asn Trp	
295 300 305	
gga tac ctc ttc aat cag aac att gca ccg gta tgg ctg gcc gaa ttc	1795
Gly Tyr Leu Phe Asn Gln Asn Ile Ala Pro Val Trp Leu Gly Glu Phe	
310 315 320	
ggt acg aca ctg caa tcc acg acc gac cag acg tgg ctg aag acg ctc	1843
Gly Thr Thr Leu Gln Ser Thr Thr Asp Gln Thr Trp Leu Lys Thr Leu	
325 330 335 340	
gtc cag tac cta cgg ccg acc gcg caa tac ggt gcg gac agc ttc cag	1891
Val Gln Tyr Leu Arg Pro Thr Ala Gln Tyr Gly Ala Asp Ser Phe Gln	
345 350 355	
tgg acc ttc tgg tcc tgg aac ccc gat tcc ggc gac aca gga gga att	1939
Trp Thr Phe Trp Ser Trp Asn Pro Asp Ser Gly Asp Thr Gly Gly Ile	
360 365 370	
ctc aag gat gac tgg cag acg gtc gac aca gta aaa gac gcc tat ctc	1987
Leu Lys Asp Asp Trp Gln Thr Val Asp Thr Val Lys Asp Gly Tyr Leu	
375 380 385	
gcg ccg atc aag tcg tcg att ttc gat cct gtc gcc gcg tct gca tcg	2035
Ala Pro Ile Lys Ser Ser Ile Phe Asp Pro Val Gly Ala Ser Ala Ser	
390 395 400	
cct agc agt caa ccg tcc ccg tcg gtg tcg ccg tct ccg tcg ccg agc	2083
Pro Ser Ser Gln Pro Ser Pro Ser Val Ser Pro Ser Pro Ser Pro Ser	
405 410 415 420	
ccg tcg gcg agt cgg acg ccg acg cct act ccg acg ccg aca gcc agc	2131
Pro Ser Ala Ser Arg Thr Pro Thr Pro Thr Pro Thr Pro Thr Ala Ser	
425 430 435	
ccg acg cca acg ctg acc cct act gct acg ccc acg ccc acg gca agc	2179
Pro Thr Pro Thr Leu Thr Pro Thr Ala Thr Pro Thr Pro Thr Ala Ser	
440 445 450	

ccg acg ccg tca ccg acg gca gcc tcc gga gcc cgc tgc acc gcg agt	2227
Pro Thr Pro Ser Pro Thr Ala Ala Ser Gly Ala Arg Cys Thr Ala Ser	
455 460 465	
tac cag gtc aac agc gat tgg ggc aat ggc ttc acg gta acg gtg gcc	2275
Tyr Gln Val Asn Ser Asp Trp Gly Asn Gly Phe Thr Val Thr Val Ala	
470 475 480	
gtg aca aat tcc gga tcc gtc gcg acc aag aca tgg acg gtc agt tgg	2323
Val Thr Asn Ser Gly Ser Val Ala Thr Lys Thr Trp Thr Val Ser Trp	
485 490 495 500	
aca ttc ggc gga aat cag acg att acc aat tcg tgg aat gca gcg gtc	2371
Thr Phe Gly Gly Asn Gln Thr Ile Thr Asn Ser Trp Asn Ala Ala Val	
505 510 515	
acg cag aac ggt cag tcg gta acg gct cgg aat atg agt tat aac aac	2419
Thr Gln Asn Gly Gln Ser Val Thr Ala Arg Asn Met Ser Tyr Asn Asn	
520 525 530	
gtg att cag cct ggt cag aac acc acg ttc gga ttc cag gcg agc tat	2467
Val Ile Gln Pro Gly Gln Asn Thr Thr Phe Gly Phe Gln Ala Ser Tyr	
535 540 545	
acc gga agc aac gcg gca ccg aca gtc gcc tgc gca gca agt taa	2512
Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala Ala Ser	
550 555 560	
tacgtcgggg agccgacggg aggggtccgga ccgtcgggttc cccggcttcc acctatggag	2572
cgaaccaaac aatccggacg gaactgcagg taccagagag gaacgacacg aatgcccgcc	2632
atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc	2692
gtgccgctgg cgatgcagca tcttgccatc gccgcgacgc acgtcgacaa tccctatgcg	2752
ggagcgacct tcttcgtcaa cccgtactgg gcgcaagaag tacagagcga acggcgaaacc	2812
agaccaatgc cactctcgca gcgaaaatgc gcgtcgtttc cacatattcg acggccgtct	2872
ggatggaccg catcgctgcg atcaacggcg tcaacggcgg acccggttg acgacatatc	2932
tggacgccgc cctctoccag cagcagggaa ccacccctga agtcattgag attgtcatct	2992
acgatctgcc gg	3004

<210> 5
 <211> 562
 <212> PRT
 <213> Acidothermus cellulolyticus

<400> 5

Val Pro Arg Ala Leu Arg Arg Val Pro Gly Ser Arg Val Met Leu Arg
1 5 10 15

Val Gly Val Val Val Ala Val Leu Ala Leu Val Ala Ala Leu Ala Asn
20 25 30

Leu Ala Val Pro Arg Pro Ala Arg Ala Ala Gly Gly Gly Tyr Trp His
35 40 45

Thr Ser Gly Arg Glu Ile Leu Asp Ala Asn Asn Val Pro Val Arg Ile
 50 55 60

Ala Gly Ile Asn Trp Phe Gly Phe Glu Thr Cys Asn Tyr Val Val His
 65 70 75 80

Gly Leu Trp Ser Arg Asp Tyr Arg Ser Met Leu Asp Gln Ile Lys Ser
 85 90 95

Leu Gly Tyr Asn Thr Ile Arg Leu Pro Tyr Ser Asp Asp Ile Leu Lys
 100 105 110

Pro Gly Thr Met Pro Asn Ser Ile Asn Phe Tyr Gln Met Asn Gln Asp
 115 120 125

Leu Gln Gly Leu Thr Ser Leu Gln Val Met Asp Lys Ile Val Ala Tyr
 130 135 140

Ala Gly Gln Ile Gly Leu Arg Ile Ile Leu Asp Arg His Arg Pro Asp
 145 150 155 160

Cys Ser Gly Gln Ser Ala Leu Trp Tyr Thr Ser Ser Val Ser Glu Ala
 165 170 175

Thr Trp Ile Ser Asp Leu Gln Ala Leu Ala Gln Arg Tyr Lys Gly Asn
 180 185 190

Pro Thr Val Val Gly Phe Asp Leu His Asn Glu Pro His Asp Pro Ala
 195 200 205

Cys Trp Gly Cys Gly Asp Pro Ser Ile Asp Trp Arg Leu Ala Ala Glu
 210 215 220

Arg Ala Gly Asn Ala Val Leu Ser Val Asn Pro Asn Leu Leu Ile Phe
 225 230 235 240

Val Glu Gly Val Gln Ser Tyr Asn Gly Asp Ser Tyr Trp Trp Gly Gly
 245 250 255

Asn Leu Gln Gly Ala Gly Gln Tyr Pro Val Val Leu Asn Val Pro Asn
 260 265 270

Arg Leu Val Tyr Ser Ala His Asp Tyr Ala Thr Ser Val Tyr Pro Gln
 275 280 285

Thr Trp Phe Ser Asp Pro Thr Phe Pro Asn Asn Met Pro Gly Ile Trp
 290 295 300

Asn Lys Asn Trp Gly Tyr Leu Phe Asn Gln Asn Ile Ala Pro Val Trp
305 310 315 320

Leu Gly Glu Phe Gly Thr Thr Leu Gln Ser Thr Thr Asp Gln Thr Trp
325 330 335

Leu Lys Thr Leu Val Gln Tyr Leu Arg Pro Thr Ala Gln Tyr Gly Ala
340 345 350

Asp Ser Phe Gln Trp Thr Phe Trp Ser Trp Asn Pro Asp Ser Gly Asp
355 360 365

Thr Gly Gly Ile Leu Lys Asp Asp Trp Gln Thr Val Asp Thr Val Lys
370 375 380

Asp Gly Tyr Leu Ala Pro Ile Lys Ser Ser Ile Phe Asp Pro Val Gly
385 390 395 400

Ala Ser Ala Ser Pro Ser Ser Gln Pro Ser Pro Ser Val Ser Pro Ser
405 410 415

Pro Ser Pro Ser Pro Ser Ala Ser Arg Thr Pro Thr Pro Thr Pro Thr
420 425 430

Pro Thr Ala Ser Pro Thr Pro Thr Leu Thr Pro Thr Ala Thr Pro Thr
435 440 445

Pro Thr Ala Ser Pro Thr Pro Ser Pro Thr Ala Ala Ser Gly Ala Arg
450 455 460

Cys Thr Ala Ser Tyr Gln Val Asn Ser Asp Trp Gly Asn Gly Phe Thr
465 470 475 480

Val Thr Val Ala Val Thr Asn Ser Gly Ser Val Ala Thr Lys Thr Trp
485 490 495

Thr Val Ser Trp Thr Phe Gly Gly Asn Gln Thr Ile Thr Asn Ser Trp
500 505 510

Asn Ala Ala Val Thr Gln Asn Gly Gln Ser Val Thr Ala Arg Asn Met
515 520 525

Ser Tyr Asn Asn Val Ile Gln Pro Gly Gln Asn Thr Thr Phe Gly Phe
530 535 540

Gln Ala Ser Tyr Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala
545 550 555 560

Ala Ser

<210> 6
<211> 1467
<212> DNA
<213> Actinomyces naeslundii

<220>
<221> CDS
<222> (1)..(1467)
<223> beta-glucosidase

<220>
<221> misc_feature
<222> (339)..(339)
<223> nucleotide is uncertain

<220>
<221> misc_feature
<222> (947)..(947)
<223> nucleotide is uncertain

<220>
<221> misc_feature
<222> (443)..(443)
<223> nucleotide is uncertain

<400> 6

atg acc gcc acg tcc act act tct aag agc aat ccg aac ttc ccc gac	48
Met Thr Ala Thr Ser Thr Thr Ser Lys Ser Asn Pro Asn Phe Pro Asp	
1 5 10 15	
ggc ttc ctg tgg ggc ggg gcc acc gcc gcc aac cag atc gag ggc gct	96
Gly Phe Leu Trp Gly Gly Ala Thr Ala Ala Asn Gln Ile Glu Gly Ala	
20 25 30	
tac aac gag gac ggc aag ggc ctg tcc gtc cag gac gtc atg cct cgg	144
Tyr Asn Glu Asp Gly Lys Gly Leu Ser Val Gln Asp Val Met Pro Arg	
35 40 45	
ggc atc atg gcc cac ccc acc cag gct ccc aca ccg gat aac ctt caa	192
Gly Ile Met Ala His Pro Thr Gln Ala Pro Thr Pro Asp Asn Leu Gln	
50 55 60	
gct cga ggc gat cga cct tct acc acc gct tac gcc gag gac atc tcc	240
Ala Arg Gly Asp Arg Pro Ser Thr Thr Ala Tyr Ala Glu Asp Ile Ser	
65 70 75 80	
ctg ttc gcg gag atg ggt ttc aag gtc ttc cgc ttc tcc atc gcc tgg	288
Leu Phe Ala Glu Met Gly Phe Lys Val Phe Arg Phe Ser Ile Ala Trp	
85 90 95	
agc cgc atc ttc ccg ctc ggc gac gag acc gag ccc aat gag gaa gga	336
Ser Arg Ile Phe Pro Leu Gly Asp Glu Thr Glu Pro Asn Glu Glu Gly	
100 105 110	
ctn gcc ttc tac gac cgg gtc ctc gac gag ctc gag aag cac ggg atc	384

Xaa	Ala	Phe	Tyr	Asp	Arg	Val	Leu	Asp	Glu	Leu	Glu	Lys	His	Gly	Ile		
	115						120					125					
gag	cca	ctg	gtc	acc	atc	agc	cac	tac	gag	acc	ccg	ctg	cac	ctg	gcg	432	
Glu	Pro	Leu	Val	Thr	Ile	Ser	His	Tyr	Glu	Thr	Pro	Leu	His	Leu	Ala		
	130					135					140						
cgc	acc	tac	gnc	ggc	tgg	acc	gac	cgc	cgc	ctc	atc	ggc	ttc	ttc	gag	480	
Arg	Thr	Tyr	Xaa	Gly	Trp	Thr	Asp	Arg	Arg	Leu	Ile	Gly	Phe	Phe	Glu		
	145				150					155					160		
cgc	tac	gcc	cgc	acc	ctg	ttc	gag	cgc	tat	ggc	aag	cgg	gtc	aag	tac	528	
Arg	Tyr	Ala	Arg	Thr	Leu	Phe	Glu	Arg	Tyr	Gly	Lys	Arg	Val	Lys	Tyr		
				165					170					175			
tgg	ctc	acc	ttc	aac	gag	atc	aac	tcc	gtg	ctc	cat	gag	ccc	ttc	cta	576	
Trp	Leu	Thr	Phe	Asn	Glu	Ile	Asn	Ser	Val	Leu	His	Glu	Pro	Phe	Leu		
			180					185					190				
tct	ggg	ggc	gtc	gcc	acg	ccc	aag	gac	agg	ccc	ccc	gag	cag	gac	ctc	624	
Ser	Gly	Gly	Val	Ala	Thr	Pro	Lys	Asp	Arg	Pro	Pro	Glu	Gln	Asp	Leu		
	195						200					205					
tac	cag	gcc	atc	caa	aac	gag	ctc	gtc	gcc	tcc	gcg	gcc	gcg	acc	agg	672	
Tyr	Gln	Ala	Ile	Gln	Asn	Glu	Leu	Val	Ala	Ser	Ala	Ala	Ala	Thr	Arg		
	210					215					220						
atc	gcc	cat	gag	acc	aac	ccc	gac	atc	cag	gtc	ggc	tgc	atg	atc	ctg	720	
Ile	Ala	His	Glu	Thr	Asn	Pro	Asp	Ile	Gln	Val	Gly	Cys	Met	Ile	Leu		
	225				230					235					240		
gcc	gat	ccc	acc	tac	ccg	ctc	acc	cct	gat	ccc	cgg	gac	gtg	tgg	gcg	768	
Ala	Asp	Pro	Thr	Tyr	Pro	Leu	Thr	Pro	Asp	Pro	Arg	Asp	Val	Trp	Ala		
				245					250					255			
gcc	aag	cag	gca	gag	cgc	gcc	aac	tac	gcc	ttc	gga	gac	ctc	cac	gta	816	
Ala	Lys	Gln	Ala	Glu	Arg	Ala	Asn	Tyr	Ala	Phe	Gly	Asp	Leu	His	Val		
			260				265						270				
cgt	ggt	gag	tac	ccc	gga	tac	ctg	cgg	cgg	acc	ctg	cgg	gac	aag	ggc	864	
Arg	Gly	Glu	Tyr	Pro	Gly	Tyr	Leu	Arg	Arg	Thr	Leu	Arg	Asp	Lys	Gly		
		275					280					285					
atc	gag	ctg	gag	atc	acc	gag	gag	gac	cgc	gtg	ctg	ctg	cgg	gag	cac	912	
Ile	Glu	Leu	Glu	Ile	Thr	Glu	Glu	Asp	Arg	Val	Leu	Leu	Arg	Glu	His		
	290					295					300						
acc	gtc	gac	ttc	gtc	tcc	ttc	tcc	tac	tac	atg	tnc	gtg	tgc	gag	acc	960	
Thr	Val	Asp	Phe	Val	Ser	Phe	Ser	Tyr	Tyr	Met	Xaa	Val	Cys	Glu	Thr		
	305				310					315					320		
gtc	acc	cag	tcg	gcc	gag	gcc	ggc	cgg	ggc	aac	ctc	atg	ggc	ggc	gtc	1008	
Val	Thr	Gln	Ser	Ala	Glu	Ala	Gly	Arg	Gly	Asn	Leu	Met	Gly	Gly	Val		
				325					330					335			
ccc	aat	ccc	acc	ctc	gag	gcc	tcc	gag	tgg	gga	tgg	cag	atc	gac	ccg	1056	
Pro	Asn	Pro	Thr	Leu	Glu	Ala	Ser	Glu	Trp	Gly	Trp	Gln	Ile	Asp	Pro		
			340					345					350				
gcg	ggc	ctg	cgc	acc	atc	ctg	aac	gac	tac	tgg	gac	cgc	tgg	ggc	aag	1104	
Ala	Gly	Leu	Arg	Thr	Ile	Leu	Asn	Asp	Tyr	Trp	Asp	Arg	Trp	Gly	Lys		
		355					360					365					
cct	ctg	ttc	atc	gtc	gag	aac	ggc	ctg	gga	gcc	aag	gac	gtc	ctc	gtt	1152	

Pro	Leu	Phe	Ile	Val	Glu	Asn	Gly	Leu	Gly	Ala	Lys	Asp	Val	Leu	Val		
370						375					380						
gac	gga	ccc	aac	ggt	ccc	acg	gtc	gag	gac	gac	tac	cgc	atc	gcc	tac	1200	
Asp	Gly	Pro	Asn	Gly	Pro	Thr	Val	Glu	Asp	Asp	Tyr	Arg	Ile	Ala	Tyr		
385					390					395				400			
atg	aac	gac	cac	ctg	gtc	cag	gtc	gcc	gag	gcc	att	gcc	gac	ggc	gtc	1248	
Met	Asn	Asp	His	Leu	Val	Gln	Val	Ala	Glu	Ala	Ile	Ala	Asp	Gly	Val		
			405					410						415			
gag	gtc	ctg	ggc	tac	acc	tcc	tgg	ggc	tgc	atc	gac	ctg	gtc	tcg	gcc	1296	
Glu	Val	Leu	Gly	Tyr	Thr	Ser	Trp	Gly	Cys	Ile	Asp	Leu	Val	Ser	Ala		
		420						425					430				
tcc	acc	gcc	cag	atg	tcc	aag	cgc	tac	ggg	ttc	atc	tac	gtg	gac	cgt	1344	
Ser	Thr	Ala	Gln	Met	Ser	Lys	Arg	Tyr	Gly	Phe	Ile	Tyr	Val	Asp	Arg		
		435					440					445					
gac	gac	ggc	ggc	aac	ggc	acc	ctg	gcc	cgc	tac	cgc	aag	aag	tcc	ttc	1392	
Asp	Asp	Gly	Gly	Asn	Gly	Thr	Leu	Ala	Arg	Tyr	Arg	Lys	Lys	Ser	Phe		
		450				455						460					
ggc	tgg	tac	cgc	gac	gtc	atc	gcc	tcc	aac	ggt	gcc	tcc	ctc	gtg	cct	1440	
Gly	Trp	Tyr	Arg	Asp	Val	Ile	Ala	Ser	Asn	Gly	Ala	Ser	Leu	Val	Pro		
465					470					475				480			
ccg	gtg	cag	gaa	ccg	ccg	cgg	ggg	tag								1467	
Pro	Val	Gln	Glu	Pro	Pro	Arg	Gly										
				485													

```

<210> 7
<211> 488
<212> PRT
<213> Actinomyces naeslundii

<220>
<221> misc_feature
<222> (113)..(113)
<223> The 'Xaa' at location 113 stands for Leu.

<220>
<221> misc_feature
<222> (148)..(148)
<223> The 'Xaa' at location 148 stands for Asp, Gly, Ala, or Val.

<220>
<221> misc_feature
<222> (316)..(316)
<223> The 'Xaa' at location 316 stands for Tyr, Cys, Ser, or Phe.

<220>
<221> misc_feature
<222> (339)..(339)
<223> nucleotide is uncertain

<220>
<221> misc_feature
<222> (947)..(947)
<223> nucleotide is uncertain

<220>
<221> misc_feature

```

<222> (443)..(443)
 <223> nucleotide is uncertain
 <400> 7

Met Thr Ala Thr Ser Thr Thr Ser Lys Ser Asn Pro Asn Phe Pro Asp
 1 5 10 15

Gly Phe Leu Trp Gly Gly Ala Thr Ala Ala Asn Gln Ile Glu Gly Ala
 20 25 30

Tyr Asn Glu Asp Gly Lys Gly Leu Ser Val Gln Asp Val Met Pro Arg
 35 40 45

Gly Ile Met Ala His Pro Thr Gln Ala Pro Thr Pro Asp Asn Leu Gln
 50 55 60

Ala Arg Gly Asp Arg Pro Ser Thr Thr Ala Tyr Ala Glu Asp Ile Ser
 65 70 75 80

Leu Phe Ala Glu Met Gly Phe Lys Val Phe Arg Phe Ser Ile Ala Trp
 85 90 95

Ser Arg Ile Phe Pro Leu Gly Asp Glu Thr Glu Pro Asn Glu Glu Gly
 100 105 110

Xaa Ala Phe Tyr Asp Arg Val Leu Asp Glu Leu Glu Lys His Gly Ile
 115 120 125

Glu Pro Leu Val Thr Ile Ser His Tyr Glu Thr Pro Leu His Leu Ala
 130 135 140

Arg Thr Tyr Xaa Gly Trp Thr Asp Arg Arg Leu Ile Gly Phe Phe Glu
 145 150 155 160

Arg Tyr Ala Arg Thr Leu Phe Glu Arg Tyr Gly Lys Arg Val Lys Tyr
 165 170 175

Trp Leu Thr Phe Asn Glu Ile Asn Ser Val Leu His Glu Pro Phe Leu
 180 185 190

Ser Gly Gly Val Ala Thr Pro Lys Asp Arg Pro Pro Glu Gln Asp Leu
 195 200 205

Tyr Gln Ala Ile Gln Asn Glu Leu Val Ala Ser Ala Ala Ala Thr Arg
 210 215 220

Ile Ala His Glu Thr Asn Pro Asp Ile Gln Val Gly Cys Met Ile Leu
 225 230 235 240

Ala Asp Pro Thr Tyr Pro Leu Thr Pro Asp Pro Arg Asp Val Trp Ala
245 250 255

Ala Lys Gln Ala Glu Arg Ala Asn Tyr Ala Phe Gly Asp Leu His Val
260 265 270

Arg Gly Glu Tyr Pro Gly Tyr Leu Arg Arg Thr Leu Arg Asp Lys Gly
275 280 285

Ile Glu Leu Glu Ile Thr Glu Glu Asp Arg Val Leu Leu Arg Glu His
290 295 300

Thr Val Asp Phe Val Ser Phe Ser Tyr Tyr Met Xaa Val Cys Glu Thr
305 310 315 320

Val Thr Gln Ser Ala Glu Ala Gly Arg Gly Asn Leu Met Gly Gly Val
325 330 335

Pro Asn Pro Thr Leu Glu Ala Ser Glu Trp Gly Trp Gln Ile Asp Pro
340 345 350

Ala Gly Leu Arg Thr Ile Leu Asn Asp Tyr Trp Asp Arg Trp Gly Lys
355 360 365

Pro Leu Phe Ile Val Glu Asn Gly Leu Gly Ala Lys Asp Val Leu Val
370 375 380

Asp Gly Pro Asn Gly Pro Thr Val Glu Asp Asp Tyr Arg Ile Ala Tyr
385 390 395 400

Met Asn Asp His Leu Val Gln Val Ala Glu Ala Ile Ala Asp Gly Val
405 410 415

Glu Val Leu Gly Tyr Thr Ser Trp Gly Cys Ile Asp Leu Val Ser Ala
420 425 430

Ser Thr Ala Gln Met Ser Lys Arg Tyr Gly Phe Ile Tyr Val Asp Arg
435 440 445

Asp Asp Gly Gly Asn Gly Thr Leu Ala Arg Tyr Arg Lys Lys Ser Phe
450 455 460

Gly Trp Tyr Arg Asp Val Ile Ala Ser Asn Gly Ala Ser Leu Val Pro
465 470 475 480

Pro Val Gln Glu Pro Pro Arg Gly
485

<210> 8
 <211> 3072
 <212> DNA
 <213> Streptococcus salivarius

<220>
 <221> CDS
 <222> (392)..(2860)
 <223> 1,6-alpha-glucanhydrolase

<400> 8

```

aactgaggcc gttgctccag tagcgacaac agaaataggt ccatcaactg ctactgttgc      60
gacagatact gcaacaacag cgacagcttc tacaatcttt tcacaagctg tgccagcaga      120
aagtgctagc tcagaaacgc ttgtagccag tgaagcacta gctcctgagt cagctgctgt      180
ggaaaccatc acatcatcat ctgataatgc tactgaagca ggacgccatt caactgctca      240
agtaacacca gttacagaag tgacagagca aaacttgaat ggtgatgcct acttgacaga      300
tccagaaaca acaaaagcag cttatagcaa gacagatggt gatattaatt attccgttgt      360
tgtgtctaat ccaacagcag aaactaagac g atg act gtc aac ttg aca ctt      412
                               Met Thr Val Asn Leu Thr Leu
                               1             5

caa cat gct tca gaa att atc ggt caa gat aac gtt gac ctt acg cta      460
Gln His Ala Ser Glu Ile Ile Gly Gln Asp Asn Val Asp Leu Thr Leu
                               10             15             20

gcg gca gga gct tca gcc aag gtt tca aac ttg aca gta gcg tca gag      508
Ala Ala Gly Ala Ser Ala Lys Val Ser Asn Leu Thr Val Ala Ser Glu
                               25             30             35

tgg ttg aca aac aat aca ggt tac ttg gtg aca atc agt gtc aac gat      556
Trp Leu Thr Asn Asn Thr Gly Tyr Leu Val Thr Ile Ser Val Asn Asp
40             45             50             55

aaa tca ggc aat gtc ttg tca agc aag cgc gct ggc ttg tct gtt gaa      604
Lys Ser Gly Asn Val Leu Ser Ser Lys Arg Ala Gly Leu Ser Val Glu
                               60             65             70

gat gat tgg aca gtt ttc cca cgt tac ggt atc gta gca ggt tca cca      652
Asp Asp Trp Thr Val Phe Pro Arg Tyr Gly Ile Val Ala Gly Ser Pro
75             80             85

act gat caa aac agt att ctt gtt aaa aat ctt gaa gcc tac cgt aaa      700
Thr Asp Gln Asn Ser Ile Leu Val Lys Asn Leu Glu Ala Tyr Arg Lys
90             95             100

gag ctt gag ctc atg aag tct atg aat atc aac tca tat ttc ttc tat      748
Glu Leu Glu Leu Met Lys Ser Met Asn Ile Asn Ser Tyr Phe Phe Tyr
105            110            115

gat gct tat aat gaa gct aca gat cct ttc cca gaa ggt gtc gat agc      796
Asp Ala Tyr Asn Glu Ala Thr Asp Pro Phe Pro Glu Gly Val Asp Ser
120            125            130            135

ttt gtt caa aaa tgg aat acc tgg agt cac act cag gtt gac act aag      844
Phe Val Gln Lys Trp Asn Thr Trp Ser His Thr Gln Val Asp Thr Lys
140            145            150

```

gct gtt aaa gaa ttg gtt gat caa gtt cat aag tca ggt gct gtt gcc Ala Val Lys Glu Leu Val Asp Gln Val His Lys Ser Gly Ala Val Ala	892
155 160 165	
atg ctt tat aac atg att tca gca gat tca aat cca aag aat ccg gcc Met Leu Tyr Asn Met Ile Ser Ala Asp Ser Asn Pro Lys Asn Pro Ala	940
170 175 180	
ctt cca ctt gct gct ttg gct tat aac ttc tac gat agc ttt ggt aag Leu Pro Leu Ala Ala Leu Ala Tyr Asn Phe Tyr Asp Ser Phe Gly Lys	988
185 190 195	
aag ggt gaa ccg atg act tac act atc ggt gat aac cca act caa gtt Lys Gly Glu Pro Met Thr Tyr Thr Ile Gly Asp Asn Pro Thr Gln Val	1036
200 205 210 215	
tac tat gat ccg gcg aat cca gat tgg caa aaa tac atc gca ggt gtc Tyr Tyr Asp Pro Ala Asn Pro Asp Trp Gln Lys Tyr Ile Ala Gly Val	1084
220 225 230	
atg aaa tca gct atg gat cgt atg gga ttc gat ggt tgg caa ggt gat Met Lys Ser Ala Met Asp Arg Met Gly Phe Asp Gly Trp Gln Gly Asp	1132
235 240 245	
aca att ggt gac aac cgt gtg act gat tat gag cac cgt aac agc aca Thr Ile Gly Asp Asn Arg Val Thr Asp Tyr Glu His Arg Asn Ser Thr	1180
250 255 260	
gac gag gct gac tca cac atg atg tct gat tca tat gcg tca ttt att Asp Glu Ala Asp Ser His Met Met Ser Asp Ser Tyr Ala Ser Phe Ile	1228
265 270 275	
aat gcc atg aag gac ctc atc ggt gaa aag tac tac atc aca atc aat Asn Ala Met Lys Asp Leu Ile Gly Glu Lys Tyr Tyr Ile Thr Ile Asn	1276
280 285 290 295	
gat gtt aat ggt ggt aat gat gat aaa cta gcc aag gca cgt caa gat Asp Val Asn Gly Gly Asn Asp Asp Lys Leu Ala Lys Ala Arg Gln Asp	1324
300 305 310	
gtt gtt tat aat gag ctt tgg aca aac ggt ggt tca gtt att cca gga Val Val Tyr Asn Glu Leu Trp Thr Asn Gly Gly Ser Val Ile Pro Gly	1372
315 320 325	
cgt atg cag gtt gcc tat ggt gat ttg aaa gca cgt atc gat atg gta Arg Met Gln Val Ala Tyr Gly Asp Leu Lys Ala Arg Ile Asp Met Val	1420
330 335 340	
cgc aat aaa act ggt aaa tca ctt atc gtt ggt gcc tac atg gaa gaa Arg Asn Lys Thr Gly Lys Ser Leu Ile Val Gly Ala Tyr Met Glu Glu	1468
345 350 355	
cca ggg att gat tat act gtt cct ggc gga aaa gca act aac ggt gct Pro Gly Ile Asp Tyr Thr Val Pro Gly Gly Lys Ala Thr Asn Gly Ala	1516
360 365 370 375	
ggt aaa gat gcc ctt gct ggt aaa cca ttg caa gct gat gcg act ctt Gly Lys Asp Ala Leu Ala Gly Lys Pro Leu Gln Ala Asp Ala Thr Leu	1564
380 385 390	
ctc gta gat gcg aca gta gct gca gca ggt ggt tat cac atg tcc att Leu Val Asp Ala Thr Val Ala Ala Ala Gly Gly Tyr His Met Ser Ile	1612
395 400 405	

cca tca gtt gac gag tta gta aac tca gca gct gtt cca gtg gcg ata 2428
Pro Ser Val Asp Glu Leu Val Asn Ser Ala Ala Val Pro Val Ala Ile
665 670 675

gct gtg tca gag acc gca cat gat aag aaa gat gac aac tca gta tct 2476
Ala Val Ser Glu Thr Ala His Asp Lys Lys Asp Asp Asn Ser Val Ser
680 685 690 695

aat acg gat caa ggt aca gta gca tca gat tca atc act aca cca gct 2524
Asn Thr Asp Gln Gly Thr Val Ala Ser Asp Ser Ile Thr Thr Pro Ala
700 705 710

tca gag gct gca agc aca gct gcc tca aca gtc tca tca gaa gta tca 2572
Ser Glu Ala Ala Ser Thr Ala Ala Ser Thr Val Ser Ser Glu Val Ser
715 720 725

gaa agt gta aca gta tca tcg gaa cca tca gaa act gaa aat agt tca 2620
Glu Ser Val Thr Val Ser Ser Glu Pro Ser Glu Thr Glu Asn Ser Ser
730 735 740

gaa gca tca act tca gag tca gca act cca acg acg aca gca att tca 2668
Glu Ala Ser Thr Ser Glu Ser Ala Thr Pro Thr Thr Thr Ala Ile Ser
745 750 755

gaa tca cat gca gta gtt gaa cca gtg gct tct ttg aca gaa tca gag 2716
Glu Ser His Ala Val Val Glu Pro Val Ala Ser Leu Thr Glu Ser Glu
760 765 770 775

agt cag gca agc act agc ctt gtt tca gaa act aca agc aca att gtc 2764
Ser Gln Ala Ser Thr Ser Leu Val Ser Glu Thr Thr Ser Thr Ile Val
780 785 790

tca gtt gct ccg tca gaa gta tca gaa agc aca tca gag gaa gtc atc 2812
Ser Val Ala Pro Ser Glu Val Ser Glu Ser Thr Ser Glu Glu Val Ile
795 800 805

ctt atg gac tat cag aaa aca tca ata gtt gga ata gac tct ctg tag 2860
Leu Met Asp Tyr Gln Lys Thr Ser Ile Val Gly Ile Asp Ser Leu
810 815 820

ctcctgcgct ctcaaaaacc ttaccaagta cttctgaaac gattacagaa gcagcatcac 2920

tcttttagcaa ctatgcaaga tattcagaaa cagcaagctc agaattctcac tctatggtag 2980

cagcttcttc agaagtttct attgaaaaat tagcagtatc tatcttgaaa gatactgagg 3040

gaggcttgta tgatgcaaca acaatcagaa at 3072

<210> 9
<211> 822
<212> PRT
<213> Streptococcus salivarius

<400> 9

Met Thr Val Asn Leu Thr Leu Gln His Ala Ser Glu Ile Ile Gly Gln
1 5 10 15

Asp Asn Val Asp Leu Thr Leu Ala Ala Gly Ala Ser Ala Lys Val Ser
20 25 30

Asn Leu Thr Val Ala Ser Glu Trp Leu Thr Asn Asn Thr Gly Tyr Leu
 35 40 45
 Val Thr Ile Ser Val Asn Asp Lys Ser Gly Asn Val Leu Ser Ser Lys
 50 55 60
 Arg Ala Gly Leu Ser Val Glu Asp Asp Trp Thr Val Phe Pro Arg Tyr
 65 70 75 80
 Gly Ile Val Ala Gly Ser Pro Thr Asp Gln Asn Ser Ile Leu Val Lys
 85 90 95
 Asn Leu Glu Ala Tyr Arg Lys Glu Leu Glu Leu Met Lys Ser Met Asn
 100 105 110
 Ile Asn Ser Tyr Phe Phe Tyr Asp Ala Tyr Asn Glu Ala Thr Asp Pro
 115 120 125
 Phe Pro Glu Gly Val Asp Ser Phe Val Gln Lys Trp Asn Thr Trp Ser
 130 135 140
 His Thr Gln Val Asp Thr Lys Ala Val Lys Glu Leu Val Asp Gln Val
 145 150 155 160
 His Lys Ser Gly Ala Val Ala Met Leu Tyr Asn Met Ile Ser Ala Asp
 165 170 175
 Ser Asn Pro Lys Asn Pro Ala Leu Pro Leu Ala Ala Leu Ala Tyr Asn
 180 185 190
 Phe Tyr Asp Ser Phe Gly Lys Lys Gly Glu Pro Met Thr Tyr Thr Ile
 195 200 205
 Gly Asp Asn Pro Thr Gln Val Tyr Tyr Asp Pro Ala Asn Pro Asp Trp
 210 215 220
 Gln Lys Tyr Ile Ala Gly Val Met Lys Ser Ala Met Asp Arg Met Gly
 225 230 235 240
 Phe Asp Gly Trp Gln Gly Asp Thr Ile Gly Asp Asn Arg Val Thr Asp
 245 250 255
 Tyr Glu His Arg Asn Ser Thr Asp Glu Ala Asp Ser His Met Met Ser
 260 265 270
 Asp Ser Tyr Ala Ser Phe Ile Asn Ala Met Lys Asp Leu Ile Gly Glu
 275 280 285

Lys Tyr Tyr Ile Thr Ile Asn Asp Val Asn Gly Gly Asn Asp Asp Lys
 290 295 300

Leu Ala Lys Ala Arg Gln Asp Val Val Tyr Asn Glu Leu Trp Thr Asn
 305 310 315 320

Gly Gly Ser Val Ile Pro Gly Arg Met Gln Val Ala Tyr Gly Asp Leu
 325 330 335

Lys Ala Arg Ile Asp Met Val Arg Asn Lys Thr Gly Lys Ser Leu Ile
 340 345 350

Val Gly Ala Tyr Met Glu Glu Pro Gly Ile Asp Tyr Thr Val Pro Gly
 355 360 365

Gly Lys Ala Thr Asn Gly Ala Gly Lys Asp Ala Leu Ala Gly Lys Pro
 370 375 380

Leu Gln Ala Asp Ala Thr Leu Leu Val Asp Ala Thr Val Ala Ala Ala
 385 390 395 400

Gly Gly Tyr His Met Ser Ile Ala Ala Leu Ala Asn Ala Asn Ala Ala
 405 410 415

Leu Asn Val Leu Gln Ser Ala Tyr Tyr Pro Thr Gln Tyr Leu Ser Val
 420 425 430

Ala Lys Asp Thr Ile Arg Lys Leu Tyr Asn Tyr Gln Gln Phe Ile Thr
 435 440 445

Ala Tyr Glu Asn Leu Leu Arg Gly Glu Gly Val Thr Asn Ser Thr Gln
 450 455 460

Ala Val Ser Thr Lys Asn Ala Ser Gly Glu Ile Leu Ser Lys Asp Ala
 465 470 475 480

Leu Gly Val Thr Gly Asp Gln Val Trp Thr Phe Ala Lys Ser Gly Lys
 485 490 495

Gly Phe Ser Thr Val Gln Met Ile Asn Met Met Gly Ile Asn Ala Gly
 500 505 510

Trp His Asn Glu Glu Gly Tyr Ala Asp Asn Lys Thr Pro Asp Ala Gln
 515 520 525

Glu Asn Leu Thr Val Arg Leu Ser Leu Ala Gly Lys Thr Ala Gln Glu
 530 535 540

Ala Ala Lys Ile Ala Asp Gln Val Tyr Val Thr Ser Pro Asp Asp Trp
545 550 555 560

Ala Thr Ser Ser Met Lys Lys Ala Gln Ala Ser Leu Glu Thr Asp Glu
565 570 575

Asn Gly Gln Pro Val Leu Val Ile Ser Val Pro Lys Leu Thr Leu Trp
580 585 590

Asn Met Leu Tyr Ile Lys Glu Asp Thr Thr Ala Thr Pro Val Glu Pro
595 600 605

Val Thr Asn Gln Ala Gly Lys Lys Val Asp Asn Thr Val Thr Ser Glu
610 615 620

Ala Ser Ser Glu Thr Ala Lys Ser Glu Asn Thr Thr Val Asn Lys Gly
625 630 635 640

Ser Glu Ala Pro Thr Asp Thr Lys Pro Ser Val Glu Ala Pro Lys Leu
645 650 655

Asp Glu Thr Thr Lys Pro Ala Pro Ser Val Asp Glu Leu Val Asn Ser
660 665 670

Ala Ala Val Pro Val Ala Ile Ala Val Ser Glu Thr Ala His Asp Lys
675 680 685

Lys Asp Asp Asn Ser Val Ser Asn Thr Asp Gln Gly Thr Val Ala Ser
690 695 700

Asp Ser Ile Thr Thr Pro Ala Ser Glu Ala Ala Ser Thr Ala Ala Ser
705 710 715 720

Thr Val Ser Ser Glu Val Ser Glu Ser Val Thr Val Ser Ser Glu Pro
725 730 735

Ser Glu Thr Glu Asn Ser Ser Glu Ala Ser Thr Ser Glu Ser Ala Thr
740 745 750

Pro Thr Thr Thr Ala Ile Ser Glu Ser His Ala Val Val Glu Pro Val
755 760 765

Ala Ser Leu Thr Glu Ser Glu Ser Gln Ala Ser Thr Ser Leu Val Ser
770 775 780

Glu Thr Thr Ser Thr Ile Val Ser Val Ala Pro Ser Glu Val Ser Glu
785 790 795 800

Ser Thr Ser Glu Glu Val Ile Leu Met Asp Tyr Gln Lys Thr Ser Ile
805 810 815

Val Gly Ile Asp Ser Leu
820

<210> 10
<211> 2220
<212> DNA
<213> *Trichoderma longibrachiatum*

<400> 10

aagggttagcc aagaacaata gccgataaag atagcctcat taaacggaat gagctagtag 60
gcaaagtcag cgaatgtgta tatataaagg ttcgagggtcc gtgcctccct catgctctcc 120
ccatctactc atcaactcag atcctccagg agacttgtac accatctttt gaggcacaga 180
aacccaatag tcaaccgcgg actggcatca tgtatcgga gttggccgtc atcacggcct 240
tcttgggcac agctcgtgct cagtcggcct gcactctcca atcgggagact caccgcctc 300
tgacatggca gaaatgctcg tctggtggca cttgcactca acagacaggc tccgtggtca 360
tcgacgcaa ctggcgctgg actcacgcta cgaacagcag cacgaactgc tacgatggca 420
acacttgagg ctcgacccta tgtcctgaca acgagacctg cggaagaac tgctgtctgg 480
acggtgcgcg ctacgcgtcc acgtacggag ttaccacgag cggtaacagc ctctccattg 540
gctttgtcac ccagtctgcg cagaagaacg ttggcgctcg cctttacctt atggcgagcg 600
acacgaccta ccaggaattc accctgcttg gcaacgagtt ctctttcgat gttgatgttt 660
cgagctgcc gtaagtgact taccatgaac ccctgacgta tcttcttggt ggctcccagc 720
tgactggcca atttaagggt cggcttgaac ggagctctct acttcgtgtc catggacgcg 780
gatggtggcg tgagcaagta tcccaccaac aacgctggcg ccaagtacgg cacggggtac 840
tgtgacagcc agtgtccccg cgatctgaag ttcatcaatg gccaggccaa cgttgagggc 900
tgggagcgt catccaacaa cgcaaacacg ggcattggag gacacggaag ctgctgctct 960
gagatggata tctgggaggc caactccatc tccgaggctc ttaccccca cccttgacg 1020
actgtcggcc aggagatctg cgagggtgat gggtcggcg gaacttactc cgataacaga 1080
tatggcgga cttgcgatcc cgatggctgc gactggaacc cataccgctt gggcaacacc 1140
agcttctacg gccctggctc aagctttacc ctcgatacca ccaagaaatt gaccgttgct 1200
accagttcg agacgtcggg tgccatcaac cgatactatg tccagaatgg cgtcactttc 1260
cagcagccca acgccgagct tggtagttag tctggcaacg agctcaacga tgattactgc 1320
acagctgagg agacagaatt cggcggtatc ctttctcaga caagggcggc ctgactcagt 1380
tcaagaaggc tacctctggc ggcattggtc tggatcatgag tctgtgggat gatgtgagtt 1440

tgatggacaa	acatgcgcgt	tgacaaagag	tcaagcagct	gactgagatg	ttacagtact	1500
acgccaacat	gctgtggctg	gactccacct	acccgacaaa	cgagacctcc	tccacaccog	1560
gtgccgtgcg	cggaagctgc	tccaccagct	ccggtgtccc	tgctcaggtc	gaatctcagt	1620
ctcccaacgc	caaggtcacc	ttctccaaca	tcaagttcgg	accatttggc	agcaccggca	1680
accctagcgg	cggcaaccct	cccggcggaa	accgtggcac	caccaccacc	cgccgcccag	1740
ccactaccac	tggaagctct	cccggaacct	cccagtctca	ctacggccag	tgcggcggta	1800
ttggctacag	cggccccacg	gtctgcgcga	gcggcacaa	ttgccaggtc	ctgaaccctt	1860
actactctca	gtgcctgtaa	agctccgtgc	gaaagcctga	cgcaccggta	gattcttgggt	1920
gagcccgat	catgacggcg	gcgggagcta	catggccccg	ggtgatttat	tttttttgta	1980
tctactttctg	acccttttca	aatatacggg	caactcatct	ttcactggag	atgcggcctg	2040
cttgggtattg	cgatgttgct	agcttggcaa	attgtggctt	tcgaaaacac	aaaacgattc	2100
cttagtagcc	atgcatttta	agataacgga	atagaagaaa	gaggaaatta	aaaaaaaaaa	2160
aaaaacaaac	atcccgttca	taaccgtag	aatcgccgct	cttcgtgtat	ccagtagcca	2220

```
<210> 11
<211> 1263
<212> DNA
<213> Phanerochaete chrysosporium
```

Gln	Gly	Lys	Phe	Gly	Gly	Gly	Gly	Ala	Asp	Gly	Ser	Ile	Ile	Thr	Phe		
		90						95					100				
tcc	tcg	atc	gag	acc	acg	tac	cac	ccg	aac	atc	ggc	ctc	gac	gag	gtc		390
Ser	Ser	Ile	Glu	Thr	Thr	Tyr	His	Pro	Asn	Ile	Gly	Leu	Asp	Glu	Val		
	105					110				115							
gtc	gcc	atc	cag	aag	ccg	ttc	atc	gcg	aag	cac	ggc	gtc	acc	cgt	ggc		438
Val	Ala	Ile	Gln	Lys	Pro	Phe	Ile	Ala	Lys	His	Gly	Val	Thr	Arg	Gly		
	120				125				130						135		
gac	ttc	atc	gca	ttc	gct	ggc	gtc	ggc	gtg	agc	aac	tgc	ccg	ggc			486
Asp	Phe	Ile	Ala	Phe	Ala	Gly	Ala	Val	Gly	Val	Ser	Asn	Cys	Pro	Gly		
				140					145					150			
gcg	ccg	cag	atg	cag	ttc	ttc	ctt	ggc	cgc	ccc	gag	gca	acg	cag	gcc		534
Ala	Pro	Gln	Met	Gln	Phe	Phe	Leu	Gly	Arg	Pro	Glu	Ala	Thr	Gln	Ala		
			155					160					165				
gcc	ccc	gac	ggc	ctc	gtg	ccc	gag	ccc	ttc	cac	acc	atc	gat	cag	gtt		582
Ala	Pro	Asp	Gly	Leu	Val	Pro	Glu	Pro	Phe	His	Thr	Ile	Asp	Gln	Val		
		170					175					180					
ctc	gct	cgc	atg	ctt	gac	gct	ggc	ggc	ttc	gac	gag	atc	gag	act	gtc		630
Leu	Ala	Arg	Met	Leu	Asp	Ala	Gly	Gly	Phe	Asp	Glu	Ile	Glu	Thr	Val		
	185					190					195						
tgg	ctg	ctc	tct	gcc	cac	tcc	atc	gcg	gct	gcg	aac	gac	gtc	gac	ccg		678
Trp	Leu	Leu	Ser	Ala	His	Ser	Ile	Ala	Ala	Ala	Asn	Asp	Val	Asp	Pro		
	200				205					210					215		
acc	atc	tcc	ggc	ctg	ccg	ttc	gac	tcc	act	ccc	ggc	cag	ttc	gac	tcc		726
Thr	Ile	Ser	Gly	Leu	Pro	Phe	Asp	Ser	Thr	Pro	Gly	Gln	Phe	Asp	Ser		
				220					225					230			
cag	ttc	ttc	gtc	gag	acg	cag	ctc	cgc	ggc	acc	gca	ttc	cct	ggc	aag		774
Gln	Phe	Phe	Val	Glu	Thr	Gln	Leu	Arg	Gly	Thr	Ala	Phe	Pro	Gly	Lys		
			235					240					245				
act	ggc	atc	cag	ggc	acc	gtc	atg	tcc	ccg	ctc	aag	ggc	gag	atg	cgt		822
Thr	Gly	Ile	Gln	Gly	Thr	Val	Met	Ser	Pro	Leu	Lys	Gly	Glu	Met	Arg		
		250				255						260					
ctg	cag	acg	gac	cac	ttg	ttc	gcg	cgt	gac	tcg	cgc	acg	gca	tgc	gag		870
Leu	Gln	Thr	Asp	His	Leu	Phe	Ala	Arg	Asp	Ser	Arg	Thr	Ala	Cys	Glu		
	265					270					275						
tgg	cag	tcc	ttc	gtc	aac	aac	cag	acg	aag	ctg	cag	gag	gac	ttc	cag		918
Trp	Gln	Ser	Phe	Val	Asn	Asn	Gln	Thr	Lys	Leu	Gln	Glu	Asp	Phe	Gln		
	280				285				290						295		
ttc	atc	ttc	acg	gcg	ctc	tcg	acg	ctc	ggc	cac	gac	atg	aac	gcc	atg		966
Phe	Ile	Phe	Thr	Ala	Leu	Ser	Thr	Leu	Gly	His	Asp	Met	Asn	Ala	Met		
				300					305					310			
atc	gac	tgc	tcc	gag	gtc	atc	ccc	gcg	ccc	aag	ccc	gtc	aac	ttc	ggc		1014
Ile	Asp	Cys	Ser	Glu	Val	Ile	Pro	Ala	Pro	Lys	Pro	Val	Asn	Phe	Gly		
			315					320					325				
ccg	tcg	ttc	ttc	ccc	gcc	ggc	aag	acg	cac	gcc	gac	atc	gag	cag	gcc		1062
Pro	Ser	Phe	Phe	Pro	Ala	Gly	Lys	Thr	His	Ala	Asp	Ile	Glu	Gln	Ala		
		330				335						340					
tgc	gca	tcc	acg	ccg	ttc	ccg	acg	ctc	atc	acc	gcc	ccc	ggc	ccc	tct		1110

Cys Ala Ser Thr Pro Phe Pro Thr Leu Ile Thr Ala Pro Gly Pro Ser
 345 350 355
 gcg tcc gtc gct cgc atc ccc ccg ccg ccg tcc ccc aac taa 1152
 Ala Ser Val Ala Arg Ile Pro Pro Pro Pro Ser Pro Asn
 360 365 370
 gctatgtcta tgctggacat gctctcggtt ctacctcgtc ggtatcgtcg cacggttatac 1212
 tcgcgtttgc atcatgtata cctgctcgtg gaatatacaa agtggcttat c 1263

<210> 12
 <211> 372
 <212> PRT
 <213> Phanerochaete chrysosporium

<400> 12

Met Ala Phe Lys Gln Leu Leu Ala Ala Leu Ser Val Ala Leu Thr Leu
 1 5 10 15

Gln Val Thr Gln Ala Ala Pro Asn Leu Asp Lys Arg Val Ala Cys Pro
 20 25 30

Asp Gly Val His Thr Ala Ser Asn Ala Ala Cys Cys Ala Trp Phe Pro
 35 40 45

Val Leu Asp Asp Ile Gln Gln Asn Leu Phe His Gly Gly Gln Cys Gly
 50 55 60

Ala Glu Ala His Glu Ala Leu Arg Met Val Phe His Asp Ser Ile Ala
 65 70 75 80

Ile Ser Pro Lys Leu Gln Ser Gln Gly Lys Phe Gly Gly Gly Gly Ala
 85 90 95

Asp Gly Ser Ile Ile Thr Phe Ser Ser Ile Glu Thr Thr Tyr His Pro
 100 105 110

Asn Ile Gly Leu Asp Glu Val Val Ala Ile Gln Lys Pro Phe Ile Ala
 115 120 125

Lys His Gly Val Thr Arg Gly Asp Phe Ile Ala Phe Ala Gly Ala Val
 130 135 140

Gly Val Ser Asn Cys Pro Gly Ala Pro Gln Met Gln Phe Phe Leu Gly
 145 150 155 160

Arg Pro Glu Ala Thr Gln Ala Ala Pro Asp Gly Leu Val Pro Glu Pro
 165 170 175

Phe His Thr Ile Asp Gln Val Leu Ala Arg Met Leu Asp Ala Gly Gly

180 185 190

Phe Asp Glu Ile Glu Thr Val Trp Leu Leu Ser Ala His Ser Ile Ala
195 200 205

Ala Ala Asn Asp Val Asp Pro Thr Ile Ser Gly Leu Pro Phe Asp Ser
210 215 220

Thr Pro Gly Gln Phe Asp Ser Gln Phe Phe Val Glu Thr Gln Leu Arg
225 230 235 240

Gly Thr Ala Phe Pro Gly Lys Thr Gly Ile Gln Gly Thr Val Met Ser
245 250 255

Pro Leu Lys Gly Glu Met Arg Leu Gln Thr Asp His Leu Phe Ala Arg
260 265 270

Asp Ser Arg Thr Ala Cys Glu Trp Gln Ser Phe Val Asn Asn Gln Thr
275 280 285

Lys Leu Gln Glu Asp Phe Gln Phe Ile Phe Thr Ala Leu Ser Thr Leu
290 295 300

Gly His Asp Met Asn Ala Met Ile Asp Cys Ser Glu Val Ile Pro Ala
305 310 315 320

Pro Lys Pro Val Asn Phe Gly Pro Ser Phe Phe Pro Ala Gly Lys Thr
325 330 335

His Ala Asp Ile Glu Gln Ala Cys Ala Ser Thr Pro Phe Pro Thr Leu
340 345 350

Ile Thr Ala Pro Gly Pro Ser Ala Ser Val Ala Arg Ile Pro Pro Pro
355 360 365

Pro Ser Pro Asn
370

<210> 13
<211> 1285
<212> DNA
<213> Phanerochaete chrysosporium

<220>
<221> CDS
<222> (34)..(1149) <223> CKG5 ligninase precursor

<400> 13

gtcagactct ccaacggttg cctttggaca gac atg gcc ttc aag aag ctc ctt
Met Ala Phe Lys Lys Leu Leu

250	255	260	
gac ttc ctg atc gct cgt gac gcg cgc acc gcc tgc gag tgg cag tcg			870
Asp Phe Leu Ile Ala Arg Asp Ala Arg Thr Ala Cys Glu Trp Gln Ser			
265	270	275	
ttc gtc aac aac cag tcc aag ctc gtc tcc gac ttc caa ttc atc ttc			918
Phe Val Asn Asn Gln Ser Lys Leu Val Ser Asp Phe Gln Phe Ile Phe			
280	285	290	295
ctc gcc ctc act cag ctc ggc cag gac ccg gat gcg atg acc gac tgc			966
Leu Ala Leu Thr Gln Leu Gly Gln Asp Pro Asp Ala Met Thr Asp Cys			
300	305	310	
tct gct gtc atc ccc atc tcc aag ccc gcc ccg aac aac acc ccc gga			1014
Ser Ala Val Ile Pro Ile Ser Lys Pro Ala Pro Asn Asn Thr Pro Gly			
315	320	325	
ttc tcc ttc ttc ccg ccc ggc atg acg atg gac gat gtc gag cag gct			1062
Phe Ser Phe Phe Pro Pro Gly Met Thr Met Asp Asp Val Glu Gln Ala			
330	335	340	
tgc gcc gag acg ccc ttc ccg act ctc tcg act ctc cct ggc ccc gcg			1110
Cys Ala Glu Thr Pro Phe Pro Thr Leu Ser Thr Leu Pro Gly Pro Ala			
345	350	355	
acc tcc gtc gct cgc atc cct cct cct cct ggt gct taa gcagccatca			1159
Thr Ser Val Ala Arg Ile Pro Pro Pro Gly Ala			
360	365	370	
gacttcggat cacaccccggt tattggcaac ggaaatttag aacgaagatc gtccagtgtt			1219
ttgaagtaga aatgtgcttg tactgtgtaa acagctcttt tgacgaaata cactctgatt			1279
tcgtcg			1285
<210> 14			
<211> 371			
<212> PRT			
<213> Phanerochaete chrysosporium			
<400> 14			
Met Ala Phe Lys Lys Leu Leu Ala Val Leu Thr Ala Ala Leu Ser Leu			
1	5	10	15
Arg Ala Ala Gln Gly Ala Ala Val Glu Lys Arg Ala Thr Cys Ser Asn			
20	25	30	
Gly Lys Val Val Pro Ala Ala Ser Cys Cys Thr Trp Phe Asn Val Leu			
35	40	45	
Ser Asp Ile Gln Glu Asn Leu Phe Asn Gly Gly Gln Cys Gly Ala Glu			
50	55	60	
Ala His Glu Ser Ile Arg Leu Val Phe His Asp Ala Ile Ala Ile Ser			
65	70	75	80

Pro Ala Met Glu Pro Gln Ala Ser Ser Val Arg Gly Ala Asp Gly Ser
 85 90 95
 Ile Met Ile Phe Asp Glu Ile Glu Thr Asn Phe His Pro Asn Ile Gly
 100 105 110
 Leu Asp Glu Ile Val Arg Leu Gln Lys Pro Phe Val Gln Lys His Gly
 115 120 125
 Val Thr Pro Gly Asp Phe Ile Ala Phe Ala Gly Ala Val Ala Leu Ser
 130 135 140
 Asn Cys Pro Gly Ala Pro Gln Met Asn Phe Phe Thr Gly Arg Ala Pro
 145 150 155 160
 Ala Thr Gln Pro Ala Pro Asp Gly Leu Val Pro Glu Pro Phe His Ser
 165 170 175
 Val Asp Gln Ile Ile Asp Arg Val Phe Asp Ala Gly Glu Phe Asp Glu
 180 185 190
 Leu Glu Leu Val Trp Met Leu Ser Ala His Ser Val Ala Ala Ala Asn
 195 200 205
 Asp Ile Asp Pro Asn Ile Gln Gly Leu Pro Phe Asp Ser Thr Pro Gly
 210 215 220
 Ile Phe Asp Ser Gln Phe Phe Val Glu Thr Gln Leu Ala Gly Thr Gly
 225 230 235 240
 Phe Thr Gly Gly Ser Asn Asn Gln Gly Glu Val Ser Ser Pro Leu Pro
 245 250 255
 Gly Glu Met Arg Leu Gln Ser Asp Phe Leu Ile Ala Arg Asp Ala Arg
 260 265 270
 Thr Ala Cys Glu Trp Gln Ser Phe Val Asn Asn Gln Ser Lys Leu Val
 275 280 285
 Ser Asp Phe Gln Phe Ile Phe Leu Ala Leu Thr Gln Leu Gly Gln Asp
 290 295 300
 Pro Asp Ala Met Thr Asp Cys Ser Ala Val Ile Pro Ile Ser Lys Pro
 305 310 315 320
 Ala Pro Asn Asn Thr Pro Gly Phe Ser Phe Phe Pro Pro Gly Met Thr
 325 330 335

Met Asp Asp Val Glu Gln Ala Cys Ala Glu Thr Pro Phe Pro Thr Leu
 340 345 350

Ser Thr Leu Pro Gly Pro Ala Thr Ser Val Ala Arg Ile Pro Pro Pro
 355 360 365

Pro Gly Ala
 370

<210> 15
 <211> 360
 <212> DNA
 <213> Solanum tuberosum

<400> 15

tgaccctaga cttgtccatc ttctggattg gccaaagttaa ttaatgtatg aaataaaaagg 60
 atgcacacat agtgacatgc taatcactat aatgtgggca tcaaagttgt gtgttatgtg 120
 taataactaa ttatctgaat aagagaaaga gagatcatcc atatttctta tcctaaatga 180
 atgacagtgt ctttataatt ctttgatgaa cagatgcatt ttattaacca attccatata 240
 catataaata ttaatcatat ataattaata tcaattgggt agcaaaaccc aaatctagtc 300
 taggtgtgtt ttgctaatta tgggggatag agcaaaaaag aaactaacgt ctcaagaatc 360

<210> 16
 <211> 2521
 <212> DNA
 <213> Agrobacterium tumefaciens

<220>
 <221> CDS
 <222> (585)..(1826)
 <223> nopaline synthetase

<400> 16

tagccgaccc agacgagcca agggatcttt ttggaatgct gctccgtcgt caggctttcc 60
 gacgtttggg tggttgaaca gaagtcatta tcgtacggaa tgccaagcac tcccgagggg 120
 aaccctgtgg ttggcatgca catacaaatg gacgaacgga taaacctttt cagccctttt 180
 taaatatccg ttattctaata aaacgctctt ttctcttagg tttaccgccc aatataatcct 240
 gtcaaacact gatagtttaa actgaaggcg ggaaacgaca atctgatcat gagcggagaa 300
 ttaaggaggat cacgttatga ccccgccga tgacgcggga caagccgttt tacgttttga 360
 actgacagaa ccgcaacgat tgaaggagcc actcagccgc gggtttctgg agtttaatga 420
 gctaagcaca tacgtcagaa accattattg cgcgttcaaa agtcgcctaa ggtcactatc 480
 agctagcaaa tatttcttgt caaaaatgct ccaactgacgt tccataaatt cccctcggta 540
 tccaattaga gtctcatatt cactctcaat ccaaataatc tgca atg gca att acc 596
 Met Ala Ile Thr

tta tcc gca act tct tta cct att tcc gcc gca gat cac cat ccg ctt Leu Ser Ala Thr Ser Leu Pro Ile Ser Ala Ala Asp His His Pro Leu 5 10 15 20	644
ccc ttg acc gta ggt gtc ctc ggt tct ggt cac gcg ggg act gca tta Pro Leu Thr Val Gly Val Leu Gly Ser Gly His Ala Gly Thr Ala Leu 25 30 35	692
gcg gct tgg ttc gcc tcc cgg cat gtt ccc acg gcg ctg tgg gca cca Ala Ala Trp Phe Ala Ser Arg His Val Pro Thr Ala Leu Trp Ala Pro 40 45 50	740
gca gat cat cca gga tcg atc tca gca atc aag gcc aat gaa gga gtt Ala Asp His Pro Gly Ser Ile Ser Ala Ile Lys Ala Asn Glu Gly Val 55 60 65	788
atc acc acc gag gga atg att aac ggt cca ttt agg gtc tca gcc tgt Ile Thr Thr Glu Gly Met Ile Asn Gly Pro Phe Arg Val Ser Ala Cys 70 75 80	836
gat gac ctt gcc gca gtt att cgc tcc agc cgt gta ctg att att gta Asp Asp Leu Ala Ala Val Ile Arg Ser Ser Arg Val Leu Ile Ile Val 85 90 95 100	884
acc cgt gcg gac gtt cac gac agc ttc gtc aac gaa ctc gcc aac ttc Thr Arg Ala Asp Val His Asp Ser Phe Val Asn Glu Leu Ala Asn Phe 105 110 115	932
aac ggc gaa ctc gca aca aag gat att gtc gtc gtg tgc ggc cat ggc Asn Gly Glu Leu Ala Thr Lys Asp Ile Val Val Val Cys Gly His Gly 120 125 130	980
ttc tcc atc aag tac gag aga cag ctg cga ttc aag cga ata ttc gag Phe Ser Ile Lys Tyr Glu Arg Gln Leu Arg Phe Lys Arg Ile Phe Glu 135 140 145	1028
acg gat aat tcg ccc ata acg tct aag cta tcg gat caa aaa aaa tgt Thr Asp Asn Ser Pro Ile Thr Ser Lys Leu Ser Asp Gln Lys Lys Cys 150 155 160	1076
aac gtc aac atc aag gaa atg aaa gcg tct ttc gga ctg tca tgt ttc Asn Val Asn Ile Lys Glu Met Lys Ala Ser Phe Gly Leu Ser Cys Phe 165 170 175 180	1124
cca att cat cgc gat gat gct ggc gtg att gat cta ccc gaa gat acc Pro Ile His Arg Asp Asp Ala Gly Val Ile Asp Leu Pro Glu Asp Thr 185 190 195	1172
aag aac atc ttt gcc cag cta ttt tcc gct aga atc atc tgc atc ccg Lys Asn Ile Phe Ala Gln Leu Phe Ser Ala Arg Ile Ile Cys Ile Pro 200 205 210	1220
ccg ttg caa gtg cta ttc ttt tcc aac tgt atc act cat gcg gtt ccg Pro Leu Gln Val Leu Phe Phe Ser Asn Cys Ile Thr His Ala Val Pro 215 220 225	1268
gca gtc atg aac atc gga aga ctc cgc gac cca gcc aat tct ctt act Ala Val Met Asn Ile Gly Arg Leu Arg Asp Pro Ala Asn Ser Leu Thr 230 235 240	1316
aaa aga gct gag aag tgg ctt ctt gaa cta gac gag cga acc cca cga Lys Arg Ala Glu Lys Trp Leu Leu Glu Leu Asp Glu Arg Thr Pro Arg	1364

245	250	255	260	
gcc gag aag ggc ttt ttc ttt tat ggt gaa gga tcc aac act tac gtt Ala Glu Lys Gly Phe Phe Phe Tyr Gly Glu Gly Ser Asn Thr Tyr Val 265 270 275				1412
tgc aac gtc caa gag caa ata gac cac gaa cgc cgg aag gtt gcc gca Cys Asn Val Gln Glu Gln Ile Asp His Glu Arg Arg Lys Val Ala Ala 280 285 290				1460
gcg tgt gga ttg cgt ctc aat tct ctc ttg cag gaa tgc aat gat gaa Ala Cys Gly Leu Arg Leu Asn Ser Leu Leu Gln Glu Cys Asn Asp Glu 295 300 305				1508
tat gat act gac tat gaa act ttg agg gaa tac tgc cta gca ccg tca Tyr Asp Thr Asp Tyr Glu Thr Leu Arg Glu Tyr Cys Leu Ala Pro Ser 310 315 320				1556
cct cat aac gtg cat cat gca tgc cct gac aac atg gaa cat cgc tat Pro His Asn Val His His Ala Cys Pro Asp Asn Met Glu His Arg Tyr 325 330 335 340				1604
ttt tct gaa gaa tta tgc tcg ttg gag gat gtc gcg gca att gca gct Phe Ser Glu Glu Leu Cys Ser Leu Glu Asp Val Ala Ala Ile Ala Ala 345 350 355				1652
att gcc aac atc gaa cta ccc ctc acg cat gca ttc atc aat att att Ile Ala Asn Ile Glu Leu Pro Leu Thr His Ala Phe Ile Asn Ile Ile 360 365 370				1700
cat gcg ggg aaa ggc aag att aat cca act ggc aaa tca tcc agc gtg His Ala Gly Lys Gly Lys Ile Asn Pro Thr Gly Lys Ser Ser Ser Val 375 380 385				1748
att ggt aac ttc agt tcc agc gac ttg att cgt ttt ggt gct acc cac Ile Gly Asn Phe Ser Ser Ser Asp Leu Ile Arg Phe Gly Ala Thr His 390 395 400				1796
gtt ttc aat aag gac gag atg gtg gag taa agaaggagtg cgtcgaagca Val Phe Asn Lys Asp Glu Met Val Glu 405 410				1846
gatcgttcaa acatttggca ataaagtttc ttaagattga atcctgttgc cggtcttgcg				1906
atgattatca tataatttct gttgaattac gttaagcatg taataattaa catgtaatgc				1966
atgacgttat ttatgagatg gggtttttatg attagagtcc cgcaattata catttaatac				2026
gcgatagaaa acaaaatata gcgcgcaaac taggataaat tatcgcgcgcg ggtgtcatct				2086
atgttactag atcgatcaaaa cttcggtact gtgtaatgac gatgagcaat cgagaggctg				2146
actaacaaaa ggtatgcccc aaaacaacct ctccaaactg tttcgaattg gaagtttctg				2206
ctcatgccga caggcataaac ttagatatc gcgggctatt ccactaatt cgtcctgctg				2266
gtttgcgcca agataaatca gtgcatctcc ttacaagttc ctctgtcttg tgaaatgaac				2326
tgctgactgc cccccaagaa agcctcctca tctccagtt ggcggcggt gatacaccat				2386
cgaaaaccca cgtccgaaca cttgatacat gtgcctgaga aataggccta cgtccaagag				2446
caagtccttt ctgtgctcgt cggaattcc tctcctgtca gacggtcgtg cgcatgtctt				2506

gcgttgatga agctt

2521

<210> 17
<211> 413
<212> PRT
<213> Agrobacterium tumefaciens

<400> 17

Met Ala Ile Thr Leu Ser Ala Thr Ser Leu Pro Ile Ser Ala Ala Asp
1 5 10 15

His His Pro Leu Pro Leu Thr Val Gly Val Leu Gly Ser Gly His Ala
20 25 30

Gly Thr Ala Leu Ala Ala Trp Phe Ala Ser Arg His Val Pro Thr Ala
35 40 45

Leu Trp Ala Pro Ala Asp His Pro Gly Ser Ile Ser Ala Ile Lys Ala
50 55 60

Asn Glu Gly Val Ile Thr Thr Glu Gly Met Ile Asn Gly Pro Phe Arg
65 70 75 80

Val Ser Ala Cys Asp Asp Leu Ala Ala Val Ile Arg Ser Ser Arg Val
85 90 95

Leu Ile Ile Val Thr Arg Ala Asp Val His Asp Ser Phe Val Asn Glu
100 105 110

Leu Ala Asn Phe Asn Gly Glu Leu Ala Thr Lys Asp Ile Val Val Val
115 120 125

Cys Gly His Gly Phe Ser Ile Lys Tyr Glu Arg Gln Leu Arg Phe Lys
130 135 140

Arg Ile Phe Glu Thr Asp Asn Ser Pro Ile Thr Ser Lys Leu Ser Asp
145 150 155 160

Gln Lys Lys Cys Asn Val Asn Ile Lys Glu Met Lys Ala Ser Phe Gly
165 170 175

Leu Ser Cys Phe Pro Ile His Arg Asp Asp Ala Gly Val Ile Asp Leu
180 185 190

Pro Glu Asp Thr Lys Asn Ile Phe Ala Gln Leu Phe Ser Ala Arg Ile
195 200 205

Ile Cys Ile Pro Pro Leu Gln Val Leu Phe Phe Ser Asn Cys Ile Thr
210 215 220

His Ala Val Pro Ala Val Met Asn Ile Gly Arg Leu Arg Asp Pro Ala
225 230 235 240

Asn Ser Leu Thr Lys Arg Ala Glu Lys Trp Leu Leu Glu Leu Asp Glu
245 250 255

Arg Thr Pro Arg Ala Glu Lys Gly Phe Phe Phe Tyr Gly Glu Gly Ser
260 265 270

Asn Thr Tyr Val Cys Asn Val Gln Glu Gln Ile Asp His Glu Arg Arg
275 280 285

Lys Val Ala Ala Ala Cys Gly Leu Arg Leu Asn Ser Leu Leu Gln Glu
290 295 300

Cys Asn Asp Glu Tyr Asp Thr Asp Tyr Glu Thr Leu Arg Glu Tyr Cys
305 310 315 320

Leu Ala Pro Ser Pro His Asn Val His His Ala Cys Pro Asp Asn Met
325 330 335

Glu His Arg Tyr Phe Ser Glu Glu Leu Cys Ser Leu Glu Asp Val Ala
340 345 350

Ala Ile Ala Ala Ile Ala Asn Ile Glu Leu Pro Leu Thr His Ala Phe
355 360 365

Ile Asn Ile Ile His Ala Gly Lys Gly Lys Ile Asn Pro Thr Gly Lys
370 375 380

Ser Ser Ser Val Ile Gly Asn Phe Ser Ser Ser Asp Leu Ile Arg Phe
385 390 395 400

Gly Ala Thr His Val Phe Asn Lys Asp Glu Met Val Glu
405 410

<210> 18

<211> 835

<212> DNA

<213> Streptomyces hygroscopicus

<400> 18

gctcgtgtc attttcgaga cgccatcttt ggaagcgggtg gccgaatccg tactgcgcgg 60

actcgacgac gcgtaaaacg atcgaccacg tacacgagtc cggacacggg gcgaggaggc 120

ccggttccgg caccgaggaa gaccgaagga agaccacacg tgagcccaga acgacgcccg 180

gccgacatcc gccgtgccac cgaggcggac atgccggcgg tctgcaccat cgtcaaccac 240

tacatcgcaga	caagcacgggt	caacttcctgt	accgagccgc	aggaaccgca	ggagtggacg	300
gacgacctcg	tccgtctgcg	ggagcgctat	ccctggctcg	tcgccgaggt	ggacggcgag	360
gtcgccggca	tcgcctacgc	gggcccctgg	aaggcacgca	acgcctacga	ctggacggcc	420
gagtcgaccg	tgtacgtctc	ccccggccac	cagcggacgg	gactgggctc	cacgctctac	480
accacactgc	tgaagtcctt	ggaggcacag	ggcttcaaga	gcgtggtcgc	tgtcatcggg	540
ctgcccacg	acccgagcgt	gcgcattgcac	gaggcgctcg	gatatgcccc	ccgcggcatg	600
ctgcggggcg	ccggcttcaa	gcacgggaac	tggcatgacg	tgggtttctg	gcagctggac	660
ttcagcctgc	cggtaccgcc	ccgtccggtc	ctgcccgtca	ccgagatctg	aacggagtgc	720
gcgtgggcat	cgcccagatt	ggagctggta	cgggaactca	tcgaactcaa	ctggcatacc	780
cgcaatggtg	aggtggaacc	gcggcggatc	gcgtacgacc	gtgccccagga	ggcct	835

```
<210> 19
<211> 623
<212> DNA
<213> Oryza sativa
```

tatatacata	cccccccctc	tctctccatc	cccccaaccc	taccaccacc	accaccacca	60
cctctctccc	cctcgctgcc	ggacgacgag	ctctctcccc	ctccccctcc	gccgcgcgcg	120
gtaaccaccc	cgcgctccctc	tctcttttct	ttctccgttt	tttttttccg	tctcgtctctg	180
atctttggcc	ttggtagttt	gggggcgaga	ggcggcttcg	tcgccagat	cggtgcgcg	240
gaggggcggg	atctcgcggc	tgggtctcgg	cgtgcggccg	gacctctcgc	gggaatgggg	300
ctctcggatg	tagatctgat	ccgccgttgt	tgggggagat	gatggggcgt	ttaaaatttc	360
gccatgctaa	acaagatcag	gaagagggga	aaagggcact	atggtttata	tttttatata	420
tttctgctgc	tgctcgtcag	gcttagatgt	gctagatctt	tctttcttct	ttttgtgggt	480
agaatttgaa	tccctcagca	ttgttcacgc	gtagtttttc	ttttcatgat	ttgtgacaaa	540
tgcagcctcg	tgcggagctt	ttttgtaggt	agaagatggc	tgacgccgag	gatgggggat	600
ccccgggtgg	tcagtccttt	atg				623

```
accatggctc aatctgcttg tactcttcaa tctgagactc atcctccact tacttggcag      60
aagtgttcac ctggtgttac ttgtactcaa cagactggat ctgttggtat tgatgctaac     120
tggagatgga ctcatgctac taactcttct actaaactgct atgatggtaa cacttgggtca     180
```

tctactcttt gtccctgataa cgagacttgt gctaagaact gctgtcttga tgggtgctgct 240
 tacgcttcta cttacggagt tactacttct ggaaactctc tttctattgg attcgttact 300
 cagtctgctc agaagaacgt tgggtgctagg ttgtacttga tggcttctga tactacttac 360
 caagagttca ctcttcttgg taacgagttc tctttcgatg ttgatgtttc tcaacttcca 420
 tgtggtttga acggagcttt gtacttcggt tctatggatg ctgatgggtg agtttctaag 480
 tatccaacta acactgctgg agctaagtat ggtactgggt actgtgattc tcagtgtcca 540
 agagatctta agttcattaa cggacaagct aatgttgagg gatgggagcc atcttctaac 600
 aatgctaaca ctggtattgg aggtcatgga tcttggttgc ctgagatgga tatttgggag 660
 gctaactcta tctctgaggc tcttactcca catccatgca ctactgttgg acaagagatt 720
 tgcgagggag atggttgtgg tggaaacttac tctgataaca gatacggagg tacttgcgat 780
 ccagatggat gtgattggaa tccatacaga cttggtaaca cttctttcta cgggtccagga 840
 tcttcattca ctcttgatac tactaagaag ttgactgttg ttactcagtt cgagacttct 900
 ggtgctatca acagatacta cgttcagaat ggagttactt tccaacaacc taacgctgag 960
 cttggttctt actctggtaa cgagttgaac gatgattact gtactgctga ggaagctgag 1020
 tttggtggat catctttctc tgataagggg ggacttactc agttcaagaa ggctacttct 1080
 ggtggtatgg ttcttggtat gtctctttgg gatgattact acgctaacat gttgtggctt 1140
 gattctactt acccaactaa cgagacttct tctactccag gtgctgttag aggatcttgc 1200
 tctacttctt ctggtgttcc tgctcaagtt gaatctcaat ctccaatgc taaggttact 1260
 ttctctaaca tcaagttcgg accaattgga tctactggta acccttctgg aggtaatcca 1320
 cctggaggta atccacctgg aactactaca actaggagac cagctactac aactggatca 1380
 tctccaggac ctactcaatc tcattacggg caatgtggag gtattgggtta ctctgggtcca 1440
 actgtttgtg cttctggaac tacttgtcaa gttcttaacc cttactattc tcaatgcctt 1500
 taatga 1506

<210> 21
 <211> 26
 <212> DNA
 <213> synthetic DNA

<220>
 <221> misc_feature
 <222> (1)..(26)
 <223> PCR primer SP1F

<400> 21

ccgcctaggc gcatggcccc ctccgt 26

<210> 22

<211> 25
<212> DNA
<213> synthetic DNA

<220>
<221> misc_feature
<222> (1)..(25)
<223> PCR primer SP3R

<400> 22

cgctgtacac gcacctgata ctgcc

25